



#3

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olsson, Lennart
Naranda, Tatjana
- (ii) TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES INVOLVED IN
MODULATION OF RESPONSE TO LIGAND BINDING
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morrison and Foerster LLP
 - (B) STREET: 755 Page Mill Road
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 10/074,695
 - (B) FILING DATE: 11-FEB-2002
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/788,820
 - (B) FILING DATE: 23-JAN-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/701,382
 - (B) FILING DATE: 22-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/612,999
 - (B) FILING DATE: 08-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Apple, Randolph T.
 - (B) REGISTRATION NUMBER: 36,429
 - (C) REFERENCE/DOCKET NUMBER: 213542000102
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 813-5933

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

Glu Arg Glu Thr Gln Ile Ala Lys Gly Asn Glu Gln Ser Phe Arg Val
1 5 10 15
Asp Leu Arg Thr Leu Leu Arg Tyr Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Thr Trp Leu Gly Arg Gln Gly Pro Glu Gly Pro Ser Ser Ile Pro Pro
1 5 10 15
Gly Thr Leu Thr Thr Leu Trp
 20

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Lys Thr Asp Ser Gln Ile Leu Lys Glu Leu Glu Glu Ser Ser Phe Arg
1 5 10 15
Lys Thr Phe Glu Asp Tyr Leu His
 20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Gly Arg Gly Asn Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser Ile
1 5 10 15
Val Leu Pro Ile Val Leu Leu Val Phe
 20 25

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg
1 5 10 15
Lys Val Phe Glu Asn Phe Leu His
 20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp Trp Met
1 5 10 15
Asn Leu Ala Glu Lys Ile Pro
 20

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Glu Lys Lys Pro Val Pro Trp Glu Ser His Asn Ser Ser Glu Thr Cys
1 5 10 15
Gly Leu Pro Thr Leu Val Gln Thr Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Thr Gly Phe Arg
1 5 10 15

Arg Ile Lys Ser Gly Ser Leu Tyr
20

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile
1 5 10 15

Gln Cys His Pro Glu Cys Leu Pro
20

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Pro Lys Thr Asp Ser Gln Ile Leu Lys Glu Leu Glu Glu Ser Ser Phe
1 5 10 15

Arg Lys Thr Phe Glu Asp Tyr Leu His Asn Val
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr
1 5 10 15

Ala Gly Gly Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu
20 25 30

Leu Arg Tyr Ala
35

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 50..1030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Glu Tyr Glu Leu Gln Tyr Lys Glu Val Asn Glu Thr Lys Trp Lys Met
1 5 10 15

Met Asp Pro Ile Leu Thr Thr Ser Val Pro Val Tyr
20 25